

COMPOSITIONS, METHODS, AND SYSTEMS FOR INFERRING BOVINE BREED

ABSTRACT OF THE DISCLOSURE

Provided herein are methods to discover and use single nucleotide polymorphisms (SNP) for identifying breed, or line and breed, or line composition of a bovine subject. The present invention further provides specific nucleic acid sequences, SNPs, and SNP patterns that can be used for identifying breed or breed combinations for Angus, Holstein, Limousin, Brahman, Hereford, Simmental, Gelbvieh, Charolais and Beefmaster breeds. These patterns can be utilized to manage animals in a feedlot to obtain optimum performance based on known characteristics of specific breeds and identify animals for breeding in selection programs. In another aspect, these patterns can be used to ensure labeling on breed specific branded products.